



SEQUENCE LISTING

<110> BIOHESION, INC.
WOODBURY, Richard
deVOS, Theo
IRANI, Meher

<120> RECOMBINANT FUSION PROTEINS WITH HIGH AFFINITY BINDING TO GOLD
AND APPLICATIONS THEREOF

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<140> US 10/671,995

<141> 2003-09-26

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<170> PatentIn version 3.3

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Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr
85           90           95

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Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr
100          105          110

```

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Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser
115          120          125

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Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser Ser Gly Ser
130          135          140

```

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Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile

```

145		150		155		160
Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser						
		165		170		175
Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His						
		180		185		190
Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys						
		195		200		205
Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln						
		210		215		220
Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln Ala Thr						
		225		230		235
Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly Pro						
		245		250		255

<210> 5
 <211> 1182
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1179)

<400> 5	
atg aga gga tcg cat cac cat cac cat cac gga tcc ggt tct ggt gcg	48
Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ala	
1 5 10 15	
caa cac gat gaa gcc gta gac aac aaa ttc aac aaa gaa caa caa aac	96
Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn	
20 25 30	
gcg ttc tat gag atc tta cat tta cct aac tta aac gaa gaa caa cga	144
Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg	
35 40 45	
aac gcc ttc atc caa agt tta aaa gat gac cca agc caa agc gct aac	192
Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn	
50 55 60	
ctt tta gca gaa gct aaa aag cta aat gat gct cag gcg ccg aaa gta	240
Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val	
65 70 75 80	
gac aac aaa ttc aac aaa gaa caa caa aac gcg ttc tat gag atc tta	288
Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu	
85 90 95	

cat tta cct aac tta aac gaa gaa caa cga aac gcc ttc atc caa agt His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser 100 105 110	336
tta aaa gat gac cca agc caa agc gct aac ctt tta gca gaa gct aaa Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys 115 120 125	384
aag cta aat gat gct cag gcg ccg aaa gta gac gcg aat tcg agc tct Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Ala Asn Ser Ser Ser 130 135 140	432
ggc agt ggc aat ggt cat atg cat gga aaa act cag gca acc agc ggg Gly Ser Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly 145 150 155 160	480
act atc cag agc atg cat gga aaa act cag gca acc agc ggg act atc Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile 165 170 175	528
cag agc atg cat gga aaa act cag gca acc agc ggg act atc cag agc Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser 180 185 190	576
atg cat gga aaa act cag gca acc agc ggg act atc cag agc atg cat Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His 195 200 205	624
gga aaa act cag gca acc agc ggg act atc cag agc atg cat gga aaa Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys 210 215 220	672
act cag gca acc agc ggg act atc cag agc atg cat gga aaa att cag Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln 225 230 235 240	720
gca acc agc ggg act atc cag agc atg cat gct ctg tcc ctc gag ggt Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly 245 250 255	768
ggc gga tcc ggt tct ggt gcg caa cac gat gaa gcc gta gac aac aaa Gly Gly Ser Gly Ser Gly Ala Gln His Asp Glu Ala Val Asp Asn Lys 260 265 270	816
ttc aac aaa gaa caa caa aac gcg ttc tat gag atc tta cat tta cct Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro 275 280 285	864
aac tta aac gaa gaa caa cga aac gcc ttc atc caa agt tta aaa gat Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp 290 295 300	912
gac cca agc caa agc gct aac ctt tta gca gaa gct aaa aag cta aat Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn 305 310 315 320	960
gat gct cag gcg ccg aaa gta gac aac aaa ttc aac aaa gaa caa caa Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln 325 330 335	1008

aac gcg ttc tat gag atc tta cat tta cct aac tta aac gaa gaa caa 1056
Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln
340 345 350

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cga aac gcc ttc atc caa agt tta aaa gat gac cca agc caa agc gct      1104
Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala
          355                      360                      365

```

aac ctt tta gca gaa gct aaa aag cta aat gat gct cag gcg ccg aaa 1152
Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
370 375 380

gta gac gcg aat tcg agc tct ggt ggc taa 1182
Val Asp Ala Asn Ser Ser Gly Gly
385 390

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<210> 6
<211> 393
<212> PRT
<213> Escherichia coli
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<400> 6

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ala
1 5 10 15

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
20 25 30

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
35 40 45

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
50 55 60

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
65 70 75 80

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
85 90 95

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
100 105 110

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
115 120 125

Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Ala Asn Ser Ser Ser
130 135 140

Gly Ser Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly

145		150		155		160
Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile	165	170	175			
Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser	180	185	190			
Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His	195	200	205			
Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys	210	215	220			
Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln	225	230	235	240		
Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly	245	250	255			
Gly Gly Ser Gly Ser Gly Ala Gln His Asp Glu Ala Val Asp Asn Lys	260	265	270			
Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro	275	280	285			
Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp	290	295	300			
Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn	305	310	315	320		
Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln	325	330	335			
Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln	340	345	350			
Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala	355	360	365			
Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys	370	375	380			
Val Asp Ala Asn Ser Ser Ser Gly Gly	385	390				

<210> 7
 <211> 1170
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1167)

<400> 7
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 Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Gly
 1 5 10 15
 cat atg gct gaa gct ggt atc acc ggc acc tgg tac aac cag ctg gga 96
 His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly
 20 25 30
 tcc acc ttc atc gtt acc gct ggt gct gac ggt gct ctg acc ggt acc 144
 Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr
 35 40 45
 tac gaa tcc gct gtt ggt aac gct gaa tct aga tac gtt ctg acc ggt 192
 Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly
 50 55 60
 cgt tac gac tcc gct ccg gct acc gac ggt tcc gga acc gct ctg ggt 240
 Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly
 65 70 75 80
 tgg acc gtt gct tgg aaa aac aac tac cgt aac gct cac tcc gct acc 288
 Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr
 85 90 95
 acc tgg tct ggc cag tac gtt ggt ggt gct gaa gct cgt atc aac acc 336
 Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr
 100 105 110
 cag tgg ttg ttg acc tcc ggc acc acc gaa gct aac gcg tgg aaa tcc 384
 Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser
 115 120 125
 acc ctg gtt ggt cac gac acc ttc acc aaa gtt tcg agc tct ggt agt 432
 Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser Ser Gly Ser
 130 135 140
 ggc aat ggt cat atg cat gga aaa act cag gca acc agc ggg act atc 480
 Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile
 145 150 155 160
 cag agc atg cat gga aaa act cag gca acc agc ggg act atc cag agc 528
 Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser
 165 170 175
 atg cat gga aaa act cag gca acc agc ggg act atc cag agc atg cat 576
 Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His
 180 185 190

gga aaa act cag gca acc agc ggg act atc cag agc atg cat gga aaa	624
Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys	
195 200 205	
act cag gca acc agc ggg act atc cag agc atg cat gga aaa act cag	672
Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln	
210 215 220	
gca acc agc ggg act atc cag agc atg cat gga aaa att cag gca acc	720
Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln Ala Thr	
225 230 235 240	
agc ggg act atc cag agc atg cat gct ctg tcc ctc gag gga tct ggt	768
Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly Ser Gly	
245 250 255	
tct ggt ggc cat atg gct gaa gct ggt atc acc ggc acc tgg tac aac	816
Ser Gly Gly His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn	
260 265 270	
cag ctg gga tcc acc ttc atc gtt acc gct ggt gct gac ggt gct ctg	864
Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu	
275 280 285	
acc ggt acc tac gaa tcc gct gtt ggt aac gct gaa tct aga tac gtt	912
Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val	
290 295 300	
ctg acc ggt cgt tac gac tcc gct ccg gct acc gac ggt tcc gga acc	960
Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr	
305 310 315 320	
gct ctg ggt tgg acc gtt gct tgg aaa aac aac tac cgt aac gct cac	1008
Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His	
325 330 335	
tcc gct acc acc tgg tct ggc cag tac gtt ggt ggt gct gaa gct cgt	1056
Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg	
340 345 350	
atc aac acc cag tgg ttg ttg acc tcc ggc acc acc gaa gct aac gcg	1104
Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala	
355 360 365	
tgg aaa tcc acc ctg gtt ggt cac gac acc ttc acc aaa gtt tcg agc	1152
Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser	
370 375 380	
tca agc tta att agc tga	1170
Ser Ser Leu Ile Ser	
385	

<210> 8
 <211> 389
 <212> PRT
 <213> Escherichia coli

<400> 8

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Gly

1	5	10	15
His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly	20	25	30
Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr	35	40	45
Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly	50	55	60
Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly	65	70	75
Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr	85	90	95
Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr	100	105	110
Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser	115	120	125
Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser Ser Gly Ser	130	135	140
Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile	145	150	155
Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser	165	170	175
Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His	180	185	190
Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys	195	200	205
Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln	210	215	220
Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln Ala Thr	225	230	235
Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly Ser Gly	245	250	255

Ser Gly Gly His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn
260 265 270

Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu
275 280 285

Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val
290 295 300

Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr
305 310 315 320

Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His
325 330 335

Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg
340 345 350

Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala
355 360 365

Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser
370 375 380

Ser Ser Leu Ile Ser
385

<210> 9
<211> 1176
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1173)

<400> 9
atg aga gga tcg cat cac cat cac cat cac gga tcc ggt tct ggt gcg 48
Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ala
1 5 10 15

caa cac gat gaa gcc gta gac aac aaa ttc aac aaa gaa caa caa aac 96
Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
20 25 30

gcg ttc tat gag atc tta cat tta cct aac tta aac gaa gaa caa cga 144
Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
35 40 45

aac gcc ttc atc caa agt tta aaa gat gac cca agc caa agc gct aac	192
Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn	
50 55 60	
ctt tta gca gaa gct aaa aag cta aat gat gct cag gcg ccg aaa gta	240
Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val	
65 70 75 80	
gac aac aaa ttc aac aaa gaa caa caa aac gcg ttc tat gag atc tta	288
Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu	
85 90 95	
cat tta cct aac tta aac gaa gaa caa cga aac gcc ttc atc caa agt	336
His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser	
100 105 110	
tta aaa gat gac cca agc caa agc gct aac ctt tta gca gaa gct aaa	384
Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys	
115 120 125	
aag cta aat gat gct cag gcg ccg aaa gta gac gcg aat tcg agc tct	432
Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Ala Asn Ser Ser Ser	
130 135 140	
ggt agt ggc aat ggt cat atg cat gga aaa act cag gca acc agc ggg	480
Gly Ser Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly	
145 150 155 160	
act atc cag agc atg cat gga aaa act cag gca acc agc ggg act atc	528
Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile	
165 170 175	
cag agc atg cat gga aaa act cag gca acc agc ggg act atc cag agc	576
Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser	
180 185 190	
atg cat gga aaa act cag gca acc agc ggg act atc cag agc atg cat	624
Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His	
195 200 205	
gga aaa act cag gca acc agc ggg act atc cag agc atg cat gga aaa	672
Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys	
210 215 220	
act cag gca acc agc ggg act atc cag agc atg cat gga aaa att cag	720
Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln	
225 230 235 240	
gca acc agc ggg act atc cag agc atg cat gct ctg tcc ctc gag gga	768
Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly	
245 250 255	
tct ggt tct ggt ggc cat atg gct gaa gct ggt atc acc ggc acc tgg	816
Ser Gly Ser Gly His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp	
260 265 270	
tac aac cag ctg gga tcc acc ttc atc gtt acc gct ggt gct gac ggt	864
Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly	
275 280 285	
gct ctg acc ggt acc tac gaa tcc gct gtt ggt aac gct gaa tct aga	912

Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg
 290 295 300

tac gtt ctg acc ggt cgt tac gac tcc gct ccg gct acc gac ggt tcc 960
 Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser
 305 310 315 320

gga acc gct ctg ggt tgg acc gtt gct tgg aaa aac aac tac cgt aac 1008
 Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn
 325 330 335

gct cac tcc gct acc acc tgg tct ggc cag tac gtt ggt ggt gct gaa 1056
 Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu
 340 345 350

gct cgt atc aac acc cag tgg ttg ttg acc tcc ggc acc acc gaa gct 1104
 Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala
 355 360 365

aac gcg tgg aaa tcc acc ctg gtt ggt cac gac acc ttc acc aaa gtt 1152
 Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val
 370 375 380

tcg agc tca agc tta att agc tga 1176
 Ser Ser Ser Ser Leu Ile Ser
 385 390

<210> 10
 <211> 391
 <212> PRT
 <213> Escherichia coli

<400> 10

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ala
 1 5 10 15

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
 20 25 30

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
 35 40 45

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
 50 55 60

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
 65 70 75 80

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
 85 90 95

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
 100 105 110

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
 115 120 125

Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Ala Asn Ser Ser Ser
 130 135 140

Gly Ser Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly
 145 150 155 160

Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile
 165 170 175

Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser
 180 185 190

Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His
 195 200 205

Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys
 210 215 220

Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln
 225 230 235 240

Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly
 245 250 255

Ser Gly Ser Gly Gly His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp
 260 265 270

Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly
 275 280 285

Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg
 290 295 300

Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser
 305 310 315 320

Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn
 325 330 335

Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu
 340 345 350

Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala
 355 360 365

Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val
 370 375 380

Ser Ser Ser Ser Leu Ile Ser
 385 390

<210> 11
 <211> 1176
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1173)

<400> 11
 atg aga gga tcg cat cac cat cac cat cac gga tcc ggt tct ggt ggc 48
 Met Arg Gly Ser His His His His His Gly Ser Gly Ser Gly Gly
 1 5 10 15
 cat atg gct gaa gct ggt atc acc ggc acc tgg tac aac cag ctg gga 96
 His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly
 20 25 30
 tcc acc ttc atc gtt acc gct ggt gct gac ggt gct ctg acc ggt acc 144
 Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr
 35 40 45
 tac gaa tcc gct gtt ggt aac gct gaa tct aga tac gtt ctg acc ggt 192
 Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly
 50 55 60
 cgt tac gac tcc gct ccg gct acc gac ggt tcc gga acc gct ctg ggt 240
 Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly
 65 70 75 80
 tgg acc gtt gct tgg aaa aac aac tac cgt aac gct cac tcc gct acc 288
 Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr
 85 90 95
 acc tgg tct ggc cag tac gtt ggt ggt gct gaa gct cgt atc aac acc 336
 Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr
 100 105 110
 cag tgg ttg ttg acc tcc ggc acc acc gaa gct aac gcg tgg aaa tcc 384
 Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser
 115 120 125
 acc ctg gtt ggt cac gac acc ttc acc aaa gtt tcg agc tct ggt agt 432
 Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser Ser Gly Ser
 130 135 140
 ggc aat ggt cat atg cat gga aaa act cag gca acc agc ggg act atc 480

385

390

<210> 12

<211> 391

<212> PRT

<213> Escherichia coli

<400> 12

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Gly
 1 5 10 15

His Met Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly
 20 25 30

Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr
 35 40 45

Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly
 50 55 60

Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly
 65 70 75 80

Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr
 85 90 95

Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr
 100 105 110

Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser
 115 120 125

Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Ser Ser Ser Gly Ser
 130 135 140

Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile
 145 150 155 160

Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser
 165 170 175

Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His
 180 185 190

Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys
 195 200 205

Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln
 210 215 220

Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile Gln Ala Thr
 225 230 235 240

Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu Gly Gly Gly
 245 250 255

Ser Gly Ser Gly Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
 260 265 270

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
 275 280 285

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
 290 295 300

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
 305 310 315 320

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 325 330 335

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
 340 345 350

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
 355 360 365

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
 370 375 380

Ala Asn Ser Ser Ser Gly Gly
 385 390

<210> 13
 <211> 393
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(390)

<400> 13
 atg aga gga tcg cat cac cat cac cat cac gga tcc gga ggt ggg agc

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Gly	Gly	Gly	Ser	
1				5					10						15	
tct	ggt	agt	ggc	aat	ggt	cat	atg	cat	gga	aaa	act	cag	gca	acc	agc	96
Ser	Gly	Ser	Gly	Asn	Gly	His	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	
			20					25					30			
ggg	act	atc	cag	agc	atg	cat	gga	aaa	act	cag	gca	acc	agc	ggg	act	144
Gly	Thr	Ile	Gln	Ser	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	
		35					40					45				
atc	cag	agc	atg	cat	gga	aaa	act	cag	gca	acc	agc	ggg	act	atc	cag	192
Ile	Gln	Ser	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	
	50					55					60					
agc	atg	cat	gga	aaa	act	cag	gca	acc	agc	ggg	act	atc	cag	agc	atg	240
Ser	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	Ser	Met	
65					70				75					80		
cat	gga	aaa	act	cag	gca	acc	agc	ggg	act	atc	cag	agc	atg	cat	gga	288
His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	Ser	Met	His	Gly	
				85				90						95		
aaa	act	cag	gca	acc	agc	ggg	act	atc	cag	agc	atg	cat	gga	aaa	att	336
Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	Ser	Met	His	Gly	Lys	Ile	
			100					105					110			
cag	gca	acc	agc	ggg	act	atc	cag	agc	atg	cat	gct	ctg	tcc	ctc	gag	384
Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	Ser	Met	His	Ala	Leu	Ser	Leu	Glu	
		115					120					125				
ggt	ccg	taa														393
Gly	Pro															
	130															

<210> 14
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 14

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Gly	Gly	Gly	Ser	
1				5					10						15	
Ser	Gly	Ser	Gly	Asn	Gly	His	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	
			20					25					30			
Gly	Thr	Ile	Gln	Ser	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	
		35					40					45				
Ile	Gln	Ser	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	
	50					55					60					
Ser	Met	His	Gly	Lys	Thr	Gln	Ala	Thr	Ser	Gly	Thr	Ile	Gln	Ser	Met	
65					70				75					80		

His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly
85 90 95

Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile
100 105 110

Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu
115 120 125

Gly Pro
130

<210> 15
<211> 741
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(738)

<400> 15
atg aga gga tcg cat cac cat cac cat cac gga tcc gga ggt ggg agc 48
Met Arg Gly Ser His His His His His His Gly Ser Gly Gly Gly Ser
1 5 10 15
tct ggt agt ggc aat ggt cat atg cat gga aaa act cag gca acc agc 96
Ser Gly Ser Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser
20 25 30
ggg act atc cag agc atg cat gga aaa act cag gca acc agc ggg act 144
Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr
35 40 45
atc cag agc atg cat gga aaa act cag gca acc agc ggg act atc cag 192
Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln
50 55 60
agc atg cat gga aaa act cag gca acc agc ggg act atc cag agc atg 240
Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met
65 70 75 80
cat gga aaa act cag gca acc agc ggg act atc cag agc atg cat gga 288
His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly
85 90 95
aaa act cag gca acc agc ggg act atc cag agc atg cat gga aaa att 336
Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile
100 105 110
cag gca acc agc ggg act atc cag agc atg cat gct ctg tcc ctc gag 384
Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu
115 120 125

ggt ggt gga agc tct ggt agt ggc aat ggt cat atg cat gga aaa act 432
 Gly Gly Gly Ser Ser Gly Ser Gly Asn Gly His Met His Gly Lys Thr
 130 135 140

cag gca acc agc ggg act atc cag agc atg cat gga aaa act cag gca 480
 Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala
 145 150 155 160

acc agc ggg act atc cag agc atg cat gga aaa act cag gca acc agc 528
 Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser
 165 170 175

ggg act atc cag agc atg cat gga aaa act cag gca acc agc ggg act 576
 Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr
 180 185 190

atc cag agc atg cat gga aaa act cag gca acc agc ggg act atc cag 624
 Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln
 195 200 205

agc atg cat gga aaa act cag gca acc agc ggg act atc cag agc atg 672
 Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met
 210 215 220

cat gga aaa att cag gca acc agc ggg act atc cag agc atg cat gct 720
 His Gly Lys Ile Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala
 225 230 235 240

ctg tcc ctc gag ggt ccg taa 741
 Leu Ser Leu Glu Gly Pro
 245

<210> 16
 <211> 246
 <212> PRT
 <213> Escherichia coli

<400> 16

Met Arg Gly Ser His His His His His His Gly Ser Gly Gly Gly Ser
 1 5 10 15

Ser Gly Ser Gly Asn Gly His Met His Gly Lys Thr Gln Ala Thr Ser
 20 25 30

Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr
 35 40 45

Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln
 50 55 60

Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met
 65 70 75 80

His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly

85

90

95

Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Ile
 100 105 110

Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala Leu Ser Leu Glu
 115 120 125

Gly Gly Gly Ser Ser Gly Ser Gly Asn Gly His Met His Gly Lys Thr
 130 135 140

Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala
 145 150 155 160

Thr Ser Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser
 165 170 175

Gly Thr Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr
 180 185 190

Ile Gln Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln
 195 200 205

Ser Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser Met
 210 215 220

His Gly Lys Ile Gln Ala Thr Ser Gly Thr Ile Gln Ser Met His Ala
 225 230 235 240

Leu Ser Leu Glu Gly Pro
 245

<210> 17
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic construct

<400> 17

Met His Gly Lys Thr Gln Ala Thr Ser Gly Thr Ile Gln Ser
 1 5 10

<210> 18
 <211> 16
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic construct

 <400> 18
 tcgaggggtcc gtaata 16

 <210> 19
 <211> 16
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 19
 agcttattac ggaccc 16

 <210> 20
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 20
 ctggtagtgg caatgggtcat atgc 24

 <210> 21
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 21
 tatgaccatt gccactacca gagct 25

 <210> 22
 <211> 16
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 22
 gatccgggttc tgggtgc 16

 <210> 23
 <211> 12
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic construct

 <400> 23
 gcaccagaac cg 12

 <210> 24
 <211> 27
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 24
 cgcgtggaaa tccaccctgg ttggtca 27

 <210> 25
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 25
 gtgtcgtgac caaccagggt ggatttcca 29

 <210> 26
 <211> 27
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 26
 cgacaccttc accaaagttt cgagctc 27

 <210> 27
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic construct

 <400> 27
 agcttgagct cgaaactttg gtgaag 26

 <210> 28
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>

<223> Synthetic construct

<400> 28

gatccggttc tggtggcca

19

<210> 29

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic construct

<400> 29

tatggccacc agaaccg

17

<210> 30

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic construct

<400> 30

Ser Ser Ser Ser Ile Leu Ser

1

5